



Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 08:04 pm BST

PDB ID : 1NOM
Title : DNA POLYMERASE BETA (POL B) (E.C.2.7.7.7), 31-KD DOMAIN;
SOAKED IN THE PRESENCE OF MNCL2 (5 MILLIMOLAR)
Authors : Pelletier, H.; Sawaya, M.R.
Deposited on : 1996-04-19
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

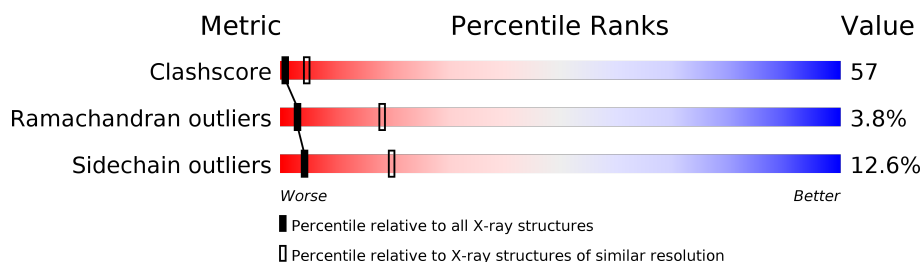
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	248	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2046 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA POLYMERASE BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	242	Total	C	N	O	S	4	1	0
			1939	1221	343	367	8			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		

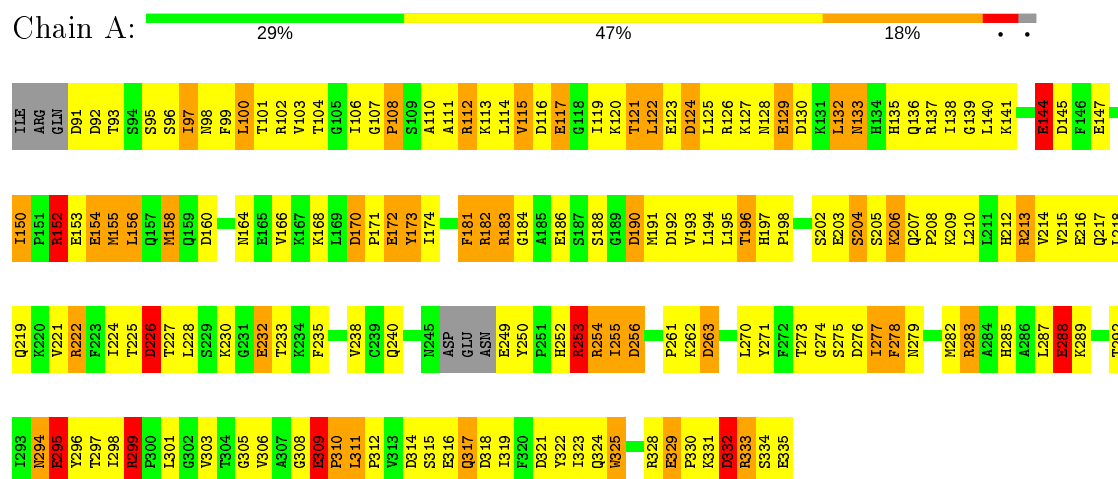
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	106	Total	O	0	0
			106	106		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: DNA POLYMERASE BETA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	120.18Å 62.88Å 38.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 43.44 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.0 (20.00-3.00) 87.8 (43.44-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.61Å)	Xtriage
Refinement program	TNT 5-D	Depositor
R, R_{free}	(Not available) , (Not available) 0.172 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	28.4	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 192.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2046	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.12	17/1977 (0.9%)	1.71	44/2666 (1.7%)

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	154	GLU	CD-OE1	6.69	1.33	1.25
1	A	203	GLU	CD-OE1	6.40	1.32	1.25
1	A	144	GLU	CD-OE1	6.22	1.32	1.25
1	A	117	GLU	CD-OE1	6.13	1.32	1.25
1	A	309	GLU	CD-OE1	5.99	1.32	1.25
1	A	295	GLU	CD-OE1	5.93	1.32	1.25
1	A	172	GLU	CD-OE1	5.93	1.32	1.25
1	A	288	GLU	CD-OE1	5.86	1.32	1.25
1	A	147	GLU	CD-OE1	5.85	1.32	1.25
1	A	335	GLU	CD-OE1	5.78	1.32	1.25
1	A	249	GLU	CD-OE1	5.74	1.31	1.25
1	A	216	GLU	CD-OE1	5.73	1.31	1.25
1	A	232	GLU	CD-OE1	5.62	1.31	1.25
1	A	186	GLU	CD-OE1	5.54	1.31	1.25
1	A	153	GLU	CD-OE2	5.52	1.31	1.25
1	A	329	GLU	CD-OE1	5.42	1.31	1.25
1	A	129	GLU	CD-OE1	5.38	1.31	1.25

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	182	ARG	NE-CZ-NH1	9.70	125.15	120.30
1	A	263	ASP	CB-CG-OD1	-9.07	110.14	118.30
1	A	190	ASP	CB-CG-OD2	-8.79	110.38	118.30
1	A	253	ARG	NE-CZ-NH1	8.48	124.54	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	145	ASP	CB-CG-OD1	-8.44	110.70	118.30
1	A	192	ASP	CB-CG-OD1	-8.05	111.06	118.30
1	A	182	ARG	NE-CZ-NH2	-7.88	116.36	120.30
1	A	132	LEU	CB-CA-C	-7.67	95.62	110.20
1	A	145	ASP	CB-CG-OD2	7.43	124.99	118.30
1	A	263	ASP	CB-CG-OD2	7.36	124.92	118.30
1	A	213	ARG	NE-CZ-NH1	7.29	123.94	120.30
1	A	190	ASP	CB-CG-OD1	7.25	124.82	118.30
1	A	321	ASP	CB-CG-OD1	-7.21	111.81	118.30
1	A	276	ASP	CB-CG-OD2	-7.20	111.82	118.30
1	A	253	ARG	NE-CZ-NH2	-6.98	116.81	120.30
1	A	299[A]	ARG	NE-CZ-NH1	6.92	123.76	120.30
1	A	299[B]	ARG	NE-CZ-NH1	6.92	123.76	120.30
1	A	170	ASP	CB-CG-OD1	-6.90	112.09	118.30
1	A	130	ASP	CB-CG-OD1	-6.80	112.18	118.30
1	A	226	ASP	CB-CG-OD1	6.79	124.41	118.30
1	A	170	ASP	CB-CG-OD2	6.69	124.32	118.30
1	A	183	ARG	NE-CZ-NH1	6.62	123.61	120.30
1	A	256	ASP	CB-CG-OD1	-6.45	112.49	118.30
1	A	309	GLU	C-N-CD	-6.27	106.80	120.60
1	A	314	ASP	CB-CG-OD1	-6.12	112.79	118.30
1	A	226	ASP	CB-CG-OD2	-6.12	112.79	118.30
1	A	333	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	A	299[A]	ARG	NE-CZ-NH2	-6.05	117.27	120.30
1	A	299[B]	ARG	NE-CZ-NH2	-6.05	117.27	120.30
1	A	213	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	A	222	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	A	112	ARG	NE-CZ-NH1	5.85	123.22	120.30
1	A	314	ASP	CB-CG-OD2	5.78	123.50	118.30
1	A	152	ARG	N-CA-CB	5.55	120.59	110.60
1	A	333	ARG	NE-CZ-NH2	-5.49	117.55	120.30
1	A	147	GLU	CB-CA-C	5.41	121.22	110.40
1	A	278	PHE	CA-CB-CG	-5.38	100.98	113.90
1	A	130	ASP	CB-CG-OD2	5.30	123.07	118.30
1	A	254	ARG	CB-CA-C	-5.30	99.81	110.40
1	A	124	ASP	CB-CG-OD1	-5.26	113.56	118.30
1	A	283	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	A	124	ASP	CB-CG-OD2	5.19	122.97	118.30
1	A	116	ASP	CB-CG-OD2	-5.17	113.65	118.30
1	A	160	ASP	CB-CG-OD1	-5.16	113.66	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1939	0	1875	218	0
2	A	1	0	0	0	0
3	A	106	0	0	11	3
All	All	2046	0	1875	218	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 57.

All (218) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:GLN:NE2	1:A:317:GLN:H	1.42	1.18
1:A:158:MET:HB2	1:A:191:MET:HE3	1.31	1.08
1:A:317:GLN:HE21	1:A:317:GLN:N	1.56	1.03
1:A:103:VAL:HB	1:A:106:ILE:HD13	1.38	1.02
1:A:294:ASN:HD22	1:A:296:TYR:H	1.02	0.93
1:A:133:ASN:HD21	1:A:135:HIS:HB3	1.33	0.92
1:A:294:ASN:ND2	1:A:296:TYR:H	1.73	0.86
1:A:122:LEU:HD12	1:A:123:GLU:N	1.91	0.85
1:A:279:ASN:O	1:A:283:ARG:HG2	1.77	0.85
1:A:103:VAL:CB	1:A:106:ILE:HD13	2.06	0.84
1:A:277:ILE:HD13	1:A:277:ILE:H	1.41	0.83
1:A:292:THR:HG22	1:A:301:LEU:HD11	1.59	0.83
1:A:138:ILE:HB	1:A:228:LEU:HD23	1.59	0.83
1:A:329:GLU:HB3	1:A:330:PRO:HD2	1.61	0.82
1:A:299[A]:ARG:HH11	1:A:299[A]:ARG:HG3	1.43	0.81
1:A:218:LEU:HA	1:A:221:VAL:CG2	2.13	0.78
1:A:292:THR:HG22	1:A:301:LEU:CD1	2.13	0.78
1:A:274:GLY:HA2	1:A:279:ASN:OD1	1.83	0.77
1:A:110:ALA:O	1:A:114:LEU:HD13	1.88	0.74
1:A:218:LEU:HA	1:A:221:VAL:HG22	1.69	0.73
1:A:150:ILE:HG12	1:A:253:ARG:HG2	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:GLN:HE21	1:A:317:GLN:H	0.78	0.72
1:A:232:GLU:HG3	1:A:233:THR:HG23	1.72	0.72
1:A:104:THR:HG22	3:A:435:HOH:O	1.88	0.71
1:A:270:LEU:HD12	1:A:333:ARG:NH1	2.05	0.71
1:A:99:PHE:O	1:A:102:ARG:HB2	1.90	0.71
1:A:138:ILE:HB	1:A:228:LEU:CD2	2.20	0.70
1:A:123:GLU:O	1:A:127:LYS:HG2	1.92	0.70
1:A:215:VAL:O	1:A:219:GLN:HG3	1.93	0.69
1:A:92:ASP:O	1:A:95:SER:HB3	1.92	0.69
1:A:170:ASP:O	1:A:173:TYR:HB2	1.94	0.68
1:A:104:THR:HG23	1:A:139:GLY:HA3	1.75	0.68
1:A:204:SER:C	1:A:206:LYS:HE2	2.14	0.68
1:A:271:TYR:CG	1:A:295:GLU:HB3	2.29	0.67
1:A:92:ASP:C	1:A:95:SER:HB3	2.15	0.67
1:A:133:ASN:ND2	1:A:135:HIS:HB3	2.06	0.67
1:A:294:ASN:OD1	1:A:299[A]:ARG:NH2	2.28	0.67
1:A:100:LEU:O	1:A:103:VAL:HG23	1.94	0.66
1:A:144:GLU:N	1:A:144:GLU:OE1	2.29	0.66
1:A:263:ASP:N	1:A:263:ASP:OD1	2.29	0.65
1:A:107:GLY:O	1:A:111:ALA:N	2.30	0.65
1:A:323:ILE:C	1:A:324:GLN:HG2	2.15	0.65
1:A:129:GLU:O	1:A:132:LEU:HB2	1.96	0.64
1:A:271:TYR:CD2	1:A:295:GLU:HB3	2.32	0.64
1:A:270:LEU:HD12	1:A:333:ARG:HH12	1.62	0.64
1:A:204:SER:CA	1:A:206:LYS:HE2	2.28	0.64
1:A:174:ILE:O	1:A:195:LEU:HD12	1.97	0.64
1:A:141:LYS:HB2	3:A:472:HOH:O	1.98	0.64
1:A:224:ILE:HD13	1:A:235:PHE:CE2	2.33	0.63
1:A:295:GLU:H	1:A:295:GLU:CD	2.02	0.62
1:A:150:ILE:HG12	1:A:253:ARG:CG	2.29	0.62
1:A:120:LYS:N	1:A:124:ASP:OD2	2.29	0.62
1:A:174:ILE:HB	1:A:196:THR:HG22	1.81	0.62
1:A:323:ILE:O	1:A:324:GLN:HG2	1.99	0.62
1:A:129:GLU:HA	1:A:132:LEU:HD12	1.80	0.62
1:A:135:HIS:ND1	1:A:228:LEU:HB3	2.14	0.62
1:A:277:ILE:HG12	1:A:278:PHE:H	1.65	0.61
1:A:301:LEU:HD12	1:A:301:LEU:N	2.15	0.61
1:A:113:LYS:HG3	1:A:114:LEU:HD12	1.81	0.61
1:A:152:ARG:NH2	1:A:181:PHE:O	2.33	0.61
1:A:278:PHE:HB2	1:A:333:ARG:O	1.99	0.61
1:A:287:LEU:HD12	1:A:287:LEU:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:MET:CB	1:A:191:MET:HE3	2.20	0.61
1:A:254:ARG:NH1	1:A:255:ILE:H	1.97	0.61
1:A:317:GLN:NE2	1:A:317:GLN:N	2.27	0.61
1:A:292:THR:CG2	1:A:301:LEU:HD11	2.31	0.60
1:A:217:GLN:HA	1:A:217:GLN:NE2	2.15	0.60
1:A:97:ILE:HD11	1:A:112:ARG:HG2	1.82	0.60
1:A:182:ARG:HD3	1:A:273:THR:CG2	2.32	0.60
1:A:224:ILE:HD13	1:A:235:PHE:HE2	1.65	0.60
1:A:283:ARG:HD3	3:A:410:HOH:O	2.01	0.60
1:A:183:ARG:NE	3:A:499:HOH:O	2.34	0.59
1:A:254:ARG:HB3	1:A:254:ARG:CZ	2.31	0.59
1:A:155:MET:HA	1:A:158:MET:HG3	1.83	0.59
1:A:193:VAL:C	1:A:194:LEU:HD12	2.22	0.59
1:A:254:ARG:NH1	1:A:254:ARG:HB3	2.18	0.59
1:A:164:ASN:O	1:A:168:LYS:HG3	2.02	0.59
1:A:315:SER:HB2	1:A:317:GLN:HE22	1.67	0.58
1:A:102:ARG:HD3	3:A:458:HOH:O	2.03	0.58
1:A:122:LEU:O	1:A:125:LEU:HB2	2.04	0.58
1:A:150:ILE:N	1:A:188:SER:O	2.28	0.58
1:A:194:LEU:HD12	1:A:194:LEU:N	2.19	0.57
1:A:289:LYS:HD2	1:A:323:ILE:O	2.04	0.57
1:A:299[B]:ARG:HD2	1:A:308:GLY:HA3	1.85	0.57
1:A:277:ILE:HD13	1:A:277:ILE:N	2.14	0.57
1:A:103:VAL:CG1	1:A:106:ILE:HD13	2.33	0.57
1:A:209:LYS:O	1:A:213:ARG:HB2	2.05	0.57
1:A:103:VAL:HB	1:A:106:ILE:CD1	2.24	0.56
1:A:150:ILE:HD11	1:A:190:ASP:HA	1.87	0.56
1:A:207:GLN:O	1:A:210:LEU:HB2	2.05	0.56
1:A:294:ASN:ND2	1:A:297:THR:H	2.04	0.56
1:A:328:ARG:NH2	3:A:470:HOH:O	2.39	0.56
1:A:182:ARG:HD3	1:A:273:THR:HG21	1.88	0.55
1:A:106:ILE:CG2	1:A:111:ALA:HB2	2.37	0.55
1:A:285:HIS:O	1:A:288:GLU:N	2.39	0.54
1:A:114:LEU:HD12	1:A:114:LEU:N	2.23	0.54
1:A:104:THR:HG23	1:A:139:GLY:CA	2.37	0.54
1:A:250:TYR:HB3	3:A:404:HOH:O	2.06	0.54
1:A:98:ASN:O	1:A:101:THR:HG22	2.07	0.54
1:A:112:ARG:O	1:A:115:VAL:HG23	2.07	0.54
1:A:135:HIS:CE1	1:A:228:LEU:HB3	2.43	0.53
1:A:254:ARG:NH1	1:A:255:ILE:N	2.56	0.53
1:A:113:LYS:HG3	1:A:114:LEU:CD1	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ARG:NH1	1:A:275:SER:N	2.56	0.53
1:A:278:PHE:CE2	1:A:282:MET:HE2	2.44	0.52
1:A:303:VAL:C	1:A:305:GLY:H	2.13	0.52
1:A:195:LEU:HG	1:A:196:THR:N	2.25	0.52
1:A:183:ARG:HD3	1:A:274:GLY:O	2.10	0.52
1:A:93:THR:O	1:A:96:SER:N	2.40	0.51
1:A:113:LYS:O	1:A:117:GLU:HG2	2.10	0.51
1:A:208:PRO:HD2	3:A:473:HOH:O	2.11	0.51
1:A:217:GLN:O	1:A:221:VAL:HG22	2.11	0.51
1:A:262:LYS:HG3	1:A:262:LYS:O	2.10	0.51
1:A:292:THR:N	1:A:301:LEU:HD11	2.26	0.51
1:A:299[A]:ARG:HG3	1:A:299[A]:ARG:NH1	2.15	0.51
1:A:270:LEU:HD22	1:A:319:ILE:HD13	1.92	0.51
1:A:97:ILE:CD1	1:A:112:ARG:HG2	2.40	0.50
1:A:334:SER:HA	3:A:499:HOH:O	2.11	0.50
1:A:108:PRO:O	1:A:112:ARG:HG3	2.12	0.50
1:A:285:HIS:CD2	1:A:325:TRP:NE1	2.80	0.50
1:A:150:ILE:O	1:A:188:SER:N	2.29	0.50
1:A:240:GLN:NE2	1:A:252:HIS:CE1	2.79	0.50
1:A:275:SER:OG	1:A:277:ILE:HG12	2.12	0.50
1:A:155:MET:HB3	1:A:181:PHE:CE2	2.47	0.49
1:A:133:ASN:ND2	1:A:136:GLN:H	2.09	0.49
1:A:100:LEU:HD11	1:A:120:LYS:O	2.13	0.49
1:A:154:GLU:O	1:A:158:MET:HG2	2.12	0.49
1:A:172:GLU:HG3	1:A:198:PRO:HG2	1.94	0.49
1:A:329:GLU:HB3	1:A:330:PRO:CD	2.38	0.49
1:A:122:LEU:HD12	1:A:123:GLU:H	1.73	0.49
1:A:127:LYS:O	1:A:128:ASN:ND2	2.46	0.49
1:A:121:THR:O	1:A:124:ASP:HB2	2.14	0.48
1:A:172:GLU:CG	1:A:198:PRO:HG2	2.43	0.48
1:A:133:ASN:ND2	1:A:136:GLN:HG3	2.29	0.48
1:A:172:GLU:HG3	1:A:198:PRO:CG	2.44	0.48
1:A:331:LYS:C	1:A:333:ARG:H	2.17	0.48
1:A:194:LEU:CD1	1:A:194:LEU:N	2.77	0.47
1:A:315:SER:HB2	1:A:317:GLN:NE2	2.29	0.47
1:A:255:ILE:HG13	1:A:256:ASP:N	2.29	0.47
1:A:285:HIS:NE2	1:A:325:TRP:CD1	2.82	0.47
1:A:297:THR:OG1	1:A:299[A]:ARG:NH1	2.47	0.47
1:A:103:VAL:O	1:A:106:ILE:N	2.47	0.47
1:A:114:LEU:CD1	1:A:114:LEU:N	2.78	0.47
1:A:277:ILE:CD1	1:A:277:ILE:H	2.09	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299[B]:ARG:HD2	1:A:308:GLY:CA	2.45	0.47
1:A:311:LEU:HA	1:A:312:PRO:HD3	1.59	0.47
1:A:104:THR:CG2	1:A:139:GLY:HA3	2.43	0.47
1:A:155:MET:CA	1:A:158:MET:HG3	2.44	0.46
1:A:311:LEU:N	1:A:311:LEU:HD13	2.30	0.46
1:A:311:LEU:CD1	1:A:311:LEU:N	2.79	0.46
1:A:126:ARG:HG2	1:A:140:LEU:HD21	1.97	0.46
1:A:202:SER:N	1:A:261:PRO:HB3	2.31	0.46
1:A:270:LEU:O	1:A:273:THR:N	2.36	0.45
1:A:278:PHE:CE2	1:A:282:MET:CE	2.98	0.45
1:A:288:GLU:N	1:A:288:GLU:OE1	2.49	0.45
1:A:212:HIS:CD2	1:A:230:LYS:HE3	2.52	0.45
1:A:319:ILE:O	1:A:323:ILE:HG12	2.17	0.45
1:A:137:ARG:NH1	3:A:468:HOH:O	2.49	0.45
1:A:218:LEU:CB	1:A:224:ILE:HG13	2.47	0.45
1:A:183:ARG:HH11	1:A:274:GLY:C	2.20	0.45
1:A:168:LYS:NZ	1:A:168:LYS:CB	2.80	0.45
1:A:218:LEU:CA	1:A:221:VAL:HG22	2.43	0.45
1:A:309:GLU:HA	1:A:310:PRO:HD3	1.65	0.45
1:A:127:LYS:C	1:A:128:ASN:HD22	2.21	0.44
1:A:101:THR:C	1:A:103:VAL:H	2.19	0.44
1:A:100:LEU:HB3	1:A:106:ILE:HG21	1.99	0.44
1:A:301:LEU:CD1	1:A:301:LEU:N	2.79	0.44
1:A:93:THR:C	1:A:96:SER:H	2.20	0.44
1:A:207:GLN:HB2	1:A:210:LEU:HD12	1.99	0.44
1:A:114:LEU:CD1	1:A:114:LEU:H	2.31	0.44
1:A:170:ASP:HA	1:A:171:PRO:HD3	1.77	0.44
1:A:182:ARG:HB3	1:A:273:THR:HG23	1.99	0.44
1:A:217:GLN:HA	1:A:217:GLN:HE21	1.81	0.44
1:A:218:LEU:O	1:A:221:VAL:HG23	2.18	0.44
1:A:137:ARG:HD3	3:A:434:HOH:O	2.18	0.43
1:A:204:SER:HB2	1:A:205:SER:H	1.44	0.43
1:A:133:ASN:HD22	1:A:135:HIS:H	1.66	0.43
1:A:227:THR:HG23	1:A:235:PHE:CE1	2.54	0.43
1:A:119:ILE:HA	1:A:124:ASP:OD2	2.18	0.43
1:A:292:THR:HG22	1:A:299[A]:ARG:O	2.19	0.43
1:A:278:PHE:CZ	1:A:282:MET:HE2	2.53	0.43
1:A:133:ASN:ND2	1:A:135:HIS:H	2.17	0.43
1:A:299[B]:ARG:HB3	1:A:308:GLY:HA2	2.01	0.43
1:A:285:HIS:CD2	1:A:325:TRP:CD1	3.06	0.43
1:A:166:VAL:CG1	1:A:173:TYR:HB3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:ARG:HA	1:A:155:MET:HB2	2.01	0.42
1:A:91:ASP:C	1:A:93:THR:H	2.21	0.42
1:A:205:SER:O	1:A:206:LYS:HB3	2.19	0.42
1:A:277:ILE:HG12	1:A:278:PHE:N	2.32	0.42
1:A:182:ARG:NH1	1:A:316:GLU:OE2	2.45	0.42
1:A:122:LEU:C	1:A:122:LEU:HD12	2.40	0.42
1:A:225:THR:OG1	1:A:238:VAL:HG12	2.19	0.42
1:A:275:SER:O	1:A:279:ASN:OD1	2.38	0.42
1:A:225:THR:O	1:A:226:ASP:OD1	2.37	0.42
1:A:330:PRO:O	1:A:333:ARG:HB2	2.20	0.42
1:A:104:THR:CG2	1:A:139:GLY:CA	2.98	0.42
1:A:133:ASN:HD22	1:A:135:HIS:N	2.17	0.41
1:A:197:HIS:CG	1:A:198:PRO:HD2	2.55	0.41
1:A:181:PHE:HB2	1:A:188:SER:OG	2.20	0.41
1:A:285:HIS:HD2	1:A:323:ILE:HD12	1.84	0.41
1:A:214:VAL:O	1:A:217:GLN:HB3	2.21	0.41
1:A:230:LYS:HB2	1:A:235:PHE:HD1	1.83	0.41
1:A:292:THR:CB	1:A:301:LEU:HD11	2.50	0.41
1:A:182:ARG:HH12	1:A:316:GLU:CD	2.23	0.41
1:A:156:LEU:CD1	1:A:181:PHE:CE2	3.04	0.41
1:A:292:THR:HG23	1:A:299[B]:ARG:HB2	2.03	0.41
1:A:210:LEU:HA	1:A:210:LEU:HD23	1.88	0.41
1:A:255:ILE:CG1	1:A:256:ASP:N	2.81	0.41
1:A:294:ASN:ND2	1:A:296:TYR:N	2.54	0.41
1:A:152:ARG:NH2	1:A:184:GLY:HA2	2.36	0.41
1:A:294:ASN:HD22	1:A:294:ASN:C	2.24	0.41
1:A:285:HIS:O	1:A:288:GLU:HB2	2.21	0.40
1:A:331:LYS:HG3	1:A:332:ASP:OD1	2.22	0.40
1:A:108:PRO:O	1:A:111:ALA:N	2.53	0.40
1:A:309:GLU:HG3	1:A:310:PRO:HD2	2.04	0.40
1:A:168:LYS:HB2	1:A:168:LYS:NZ	2.35	0.40
1:A:298:ILE:C	1:A:299[A]:ARG:HG3	2.42	0.40
1:A:318:ASP:O	1:A:322:TYR:CD2	2.74	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:477:HOH:O	3:A:477:HOH:O[2_555]	0.50	1.70
3:A:468:HOH:O	3:A:468:HOH:O[2_565]	0.71	1.49
3:A:502:HOH:O	3:A:502:HOH:O[2_555]	1.73	0.47

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	239/248 (96%)	197 (82%)	33 (14%)	9 (4%)	3	18

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	204	SER
1	A	206	LYS
1	A	309	GLU
1	A	306	VAL
1	A	108	PRO
1	A	144	GLU
1	A	222	ARG
1	A	332	ASP
1	A	310	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	207/226 (92%)	180 (87%)	27 (13%)	4	19

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	ILE
1	A	100	LEU

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Mol	Chain	Res	Type
1	A	115	VAL
1	A	121	THR
1	A	122	LEU
1	A	133	ASN
1	A	150	ILE
1	A	152	ARG
1	A	155	MET
1	A	156	LEU
1	A	158	MET
1	A	173	TYR
1	A	181	PHE
1	A	196	THR
1	A	226	ASP
1	A	253	ARG
1	A	255	ILE
1	A	277	ILE
1	A	288	GLU
1	A	294	ASN
1	A	295	GLU
1	A	299[A]	ARG
1	A	299[B]	ARG
1	A	311	LEU
1	A	317	GLN
1	A	325	TRP
1	A	332	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	ASN
1	A	133	ASN
1	A	136	GLN
1	A	157	GLN
1	A	207	GLN
1	A	217	GLN
1	A	240	GLN
1	A	252	HIS
1	A	281	ASN
1	A	285	HIS
1	A	294	ASN
1	A	317	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.